E. O'Hara

1646

#10 1-22

CRF Er[illegible]s Corrected by the STIC Systems [illegible]ranch

Serial Number: 09/376,430A

ENTERED

RECEIVED
APR 24 2000
TECH CENTER 1600/2900

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: _____
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____.
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: _____
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: _____
- ☑ Deleted: ☑ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____.
- ☐ Inserted mandatory headings, specifically: _____
- ☐ Corrected an obvious error in the response, specifically: _____
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: _____
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted ***ending*** stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____
- ☐ Other: _____

***Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.**

3/1/95

RAW SEQUENCE LISTING
PATENT APPLICATION **US/09/376,430A**

DATE: 04/06/2000
TIME: 11:23:37

Input Set: **I376430A.RAW**

This Raw Listing contains the General Information Section and up to first 5 pages.

P.5

<110> APPLICANT: Moore, Paul A.
Rosen, Craig A.
Ruben, Steven M.
<120> TITLE OF INVENTION: Cytokine Receptor Common Gamma Chain Like
<130> FILE REFERENCE: PF466P1
<140> CURRENT APPLICATION NUMBER: US/09/376,430A
<141> CURRENT FILING DATE: 1999-08-18
<150> EARLIER APPLICATION NUMBER: 60/086,505
<151> EARLIER FILING DATE: 1998-05-22
<150> EARLIER APPLICATION NUMBER: 60/078,563
<151> EARLIER FILING DATE: 1998-03-19
<150> EARLIER APPLICATION NUMBER: 09/263,626
<151> EARLIER FILING DATE: 1999-03-05
<150> EARLIER APPLICATION NUMBER: PCT/US99/05068
<151> EARLIER FILING DATE: 1999-03-05
<160> NUMBER OF SEQ ID NOS: 32
<170> SOFTWARE: PatentIn Ver. 2.0
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<211> LENGTH: 1573
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (13)..(1125)
<400> SEQUENCE: 1

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                    1               5                  10
ctg ctg gga ggc tgg atg gct ttg ggg caa gga gga gca gca gaa gga   99
Leu Leu Gly Gly Trp Met Ala Leu Gly Gln Gly Gly Ala Ala Glu Gly
     15                  20                  25
gta cag att cag atc atc tac ttc aat tta gaa acc gtg cag gtg aca   147
Val Gln Ile Gln Ile Ile Tyr Phe Asn Leu Glu Thr Val Gln Val Thr
 30                  35                  40                  45
tgg aat gcc agc aaa tac tcc agg acc aac ctg act ttc cac tac aga   195
Trp Asn Ala Ser Lys Tyr Ser Arg Thr Asn Leu Thr Phe His Tyr Arg
                 50                  55                  60
ttc aac ggt gat gag gcc tat gac cag tgc acc aac tac ctt ctc cag   243
Phe Asn Gly Asp Glu Ala Tyr Asp Gln Cys Thr Asn Tyr Leu Leu Gln
             65                  70                  75
gaa ggt cac act tcg ggg tgc ctc cta gac gca gag cag cga gac gac   291
Glu Gly His Thr Ser Gly Cys Leu Leu Asp Ala Glu Gln Arg Asp Asp
         80                  85                  90
att ctc tat ttc tcc atc agg aat ggg acg cac ccc gtt ttc acc gca   339
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Input Set: **I376430A.RAW**

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48          Ser Arg Trp Met Val Tyr Tyr Leu Lys Pro Ser Ser Pro Lys His Val
49          110                 115                 120                 125
50          aga ttt tcg tgg cat cag gat gca gtg acg gtg acg tgt tct gac ctg   435
51          Arg Phe Ser Trp His Gln Asp Ala Val Thr Val Thr Cys Ser Asp Leu
52                          130                 135                 140
53          tcc tac ggg gat ctc ctc tat gag gtt cag tac cgg agc ccc ttc gac   483
54          Ser Tyr Gly Asp Leu Leu Tyr Glu Val Gln Tyr Arg Ser Pro Phe Asp
55                      145                 150                 155
56          acc gag tgg cag tcc aaa cag gaa aat acc tgc aac gtc acc ata gaa   531
57          Thr Glu Trp Gln Ser Lys Gln Glu Asn Thr Cys Asn Val Thr Ile Glu
58                  160                 165                 170
59          ggc ttg gat gcc gag aag tgt tac tct ttc tgg gtc agg gtg aag gct   579
60          Gly Leu Asp Ala Glu Lys Cys Tyr Ser Phe Trp Val Arg Val Lys Ala
61              175                 180                 185
62          atg gag gat gta tat ggg cca gac aca tac cca agc gac tgg tca gag   627
63          Met Glu Asp Val Tyr Gly Pro Asp Thr Tyr Pro Ser Asp Trp Ser Glu
64          190                 195                 200                 205
65          gtg aca tgc tgg cag aga ggc gag att cgg gat gcc tgt gca gag aca   675
66          Val Thr Cys Trp Gln Arg Gly Glu Ile Arg Asp Ala Cys Ala Glu Thr
67                          210                 215                 220
68          cca acg cct ccc aaa cca aag ctg tcc aaa ttt att tta att tcc agc   723
69          Pro Thr Pro Pro Lys Pro Lys Leu Ser Lys Phe Ile Leu Ile Ser Ser
70                      225                 230                 235
71          ctg gcc atc ctt ctg atg gtg tct ctc ctc ctt ctg tct tta tgg aaa   771
72          Leu Ala Ile Leu Leu Met Val Ser Leu Leu Leu Leu Ser Leu Trp Lys
73                  240                 245                 250
74          tta tgg aga gtg aag aag ttt ctc att ccc agc gtg cca gac ccg aaa   819
75          Leu Trp Arg Val Lys Lys Phe Leu Ile Pro Ser Val Pro Asp Pro Lys
76              255                 260                 265
77          tcc atc ttc ccc ggg ctc ttt gag ata cac caa ggg aac ttc cag gag   867
78          Ser Ile Phe Pro Gly Leu Phe Glu Ile His Gln Gly Asn Phe Gln Glu
79          270                 275                 280                 285
80          tgg atc aca gac acc cag aac gtg gcc cac ctc cac aag atg gca ggt   915
81          Trp Ile Thr Asp Thr Gln Asn Val Ala His Leu His Lys Met Ala Gly
82                          290                 295                 300
83          gca gag caa gaa agt ggc ccc gag gag ccc ctg gta gtc cag ttg gcc   963
84          Ala Glu Gln Glu Ser Gly Pro Glu Glu Pro Leu Val Val Gln Leu Ala
85                      305                 310                 315
86          aag act gaa gcc gag tct ccc agg atg ctg gac cca cag acc gag gag   1011
87          Lys Thr Glu Ala Glu Ser Pro Arg Met Leu Asp Pro Gln Thr Glu Glu
88                  320                 325                 330
89          aaa gag gcc tct ggg gga tcc ctc cag ctt ccc cac cag ccc ctc caa   1059
90          Lys Glu Ala Ser Gly Gly Ser Leu Gln Leu Pro His Gln Pro Leu Gln
91              335                 340                 345
92          ggc ggt gat gtg gtc aca atc ggg ggc ttc acc ttt gtg atg aat gac   1107
93          Gly Gly Asp Val Val Thr Ile Gly Gly Phe Thr Phe Val Met Asn Asp
94          350                 355                 360                 365
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cgc tcc tac gtg gcg ttg tgatggacac accactgtca aagtcaacgt 1155
Arg Ser Tyr Val Ala Leu
370
caggatccac gttgacattt aaagacagag gggactgtcc cggggactcc acaccaccat 1215
ggatgggaag tctccacgcc aatgatggta ggactaggag actctgaaga cccagcctca 1275
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cttgatggca gatgggagcc aattgctcca ggagatttac tcccagttcc ttttcgtgcc 1395
tgaacgttgt cacataaacc ccaaggcagc acgtccaaaa tgctgtaaaa ccatcttccc 1455
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ttttttgtct gttttgagac tccaaaccac ctctacccct acaaaaaaaa aaaaaaaa 1573

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<211> LENGTH: 371
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 2

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Gly Trp Met Ala Leu Gly Gln Gly Gly Ala Ala Glu Gly Val Gln Ile
20 25 30
Gln Ile Ile Tyr Phe Asn Leu Glu Thr Val Gln Val Thr Trp Asn Ala
35 40 45
Ser Lys Tyr Ser Arg Thr Asn Leu Thr Phe His Tyr Arg Phe Asn Gly
50 55 60
Asp Glu Ala Tyr Asp Gln Cys Thr Asn Tyr Leu Leu Gln Glu Gly His
65 70 75 80
Thr Ser Gly Cys Leu Leu Asp Ala Glu Gln Arg Asp Asp Ile Leu Tyr
85 90 95
Phe Ser Ile Arg Asn Gly Thr His Pro Val Phe Thr Ala Ser Arg Trp
100 105 110
Met Val Tyr Tyr Leu Lys Pro Ser Ser Pro Lys His Val Arg Phe Ser
115 120 125
Trp His Gln Asp Ala Val Thr Val Thr Cys Ser Asp Leu Ser Tyr Gly
130 135 140
Asp Leu Leu Tyr Glu Val Gln Tyr Arg Ser Pro Phe Asp Thr Glu Trp
145 150 155 160
Gln Ser Lys Gln Glu Asn Thr Cys Asn Val Thr Ile Glu Gly Leu Asp
165 170 175
Ala Glu Lys Cys Tyr Ser Phe Trp Val Arg Val Lys Ala Met Glu Asp
180 185 190
Val Tyr Gly Pro Asp Thr Tyr Pro Ser Asp Trp Ser Glu Val Thr Cys
195 200 205
Trp Gln Arg Gly Glu Ile Arg Asp Ala Cys Ala Glu Thr Pro Thr Pro
210 215 220
Pro Lys Pro Lys Leu Ser Lys Phe Ile Leu Ile Ser Ser Leu Ala Ile
225 230 235 240
Leu Leu Met Val Ser Leu Leu Leu Leu Ser Leu Trp Lys Leu Trp Arg
245 250 255
Val Lys Lys Phe Leu Ile Pro Ser Val Pro Asp Pro Lys Ser Ile Phe
260 265 270
Pro Gly Leu Phe Glu Ile His Gln Gly Asn Phe Gln Glu Trp Ile Thr

```
                275                 280                 285
Asp Thr Gln Asn Val Ala His Leu His Lys Met Ala Gly Ala Glu Gln
    290                 295                 300
Glu Ser Gly Pro Glu Glu Pro Leu Val Val Gln Leu Ala Lys Thr Glu
305                 310                 315                 320
Ala Glu Ser Pro Arg Met Leu Asp Pro Gln Thr Glu Glu Lys Glu Ala
                325                 330                 335
Ser Gly Gly Ser Leu Gln Leu Pro His Gln Pro Leu Gln Gly Gly Asp
            340                 345                 350
Val Val Thr Ile Gly Gly Phe Thr Phe Val Met Asn Asp Arg Ser Tyr
        355                 360                 365
Val Ala Leu
    370

<210> SEQ ID NO 3
<211> LENGTH: 363
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 3
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Asn Glu Asp Ile Gly Gly Lys Pro Gly Thr Gly Gly Asp Phe Phe Leu
            20                  25                  30
Thr Ser Thr Pro Ala Gly Thr Leu Asp Val Ser Thr Leu Pro Leu Pro
        35                  40                  45
Lys Val Gln Cys Phe Val Phe Asn Val Glu Tyr Met Asn Cys Thr Trp
    50                  55                  60
Asn Ser Ser Ser Glu Pro Gln Pro Asn Asn Leu Thr Leu His Tyr Gly
65                  70                  75                  80
Tyr Arg Asn Phe Asn Gly Asp Asp Lys Leu Gln Glu Cys Gly His Tyr
                85                  90                  95
Leu Phe Ser Glu Gly Ile Thr Ser Gly Cys Trp Phe Gly Lys Lys Glu
            100                 105                 110
Ile Arg Leu Tyr Glu Thr Phe Val Val Gln Leu Gln Asp Pro Arg Glu
        115                 120                 125
His Arg Lys Gln Pro Lys Gln Met Leu Lys Leu Gln Asp Leu Val Ile
    130                 135                 140
Pro Trp Ala Pro Glu Asn Leu Thr Leu Arg Asn Leu Ser Glu Phe Gln
145                 150                 155                 160
Leu Glu Leu Ser Trp Ser Asn Arg Tyr Leu Asp His Cys Leu Glu His
                165                 170                 175
Leu Val Gln Tyr Arg Ser Asp Arg Asp Arg Ser Trp Thr Glu Gln Ser
            180                 185                 190
Val Asp His Arg His Ser Phe Ser Leu Pro Ser Val Asp Ala Gln Lys
        195                 200                 205
Leu Tyr Thr Phe Arg Val Arg Ser Arg Tyr Asn Pro Leu Cys Gly Ser
    210                 215                 220
Ala Gln His Trp Ser Asp Trp Ser Tyr Pro Ile His Trp Gly Ser Asn
225                 230                 235                 240
Thr Ser Lys Glu Asn Ile Glu Asn Pro Glu Asn Pro Ser Leu Phe Ala
                245                 250                 255
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195         Leu Glu Ala Val Leu Ile Pro Leu Gly Ser Met Gly Leu Ile Val Ser
196                     260                 265                 270
197         Leu Ile Cys Val Tyr Cys Trp Leu Glu Arg Thr Met Pro Arg Ile Pro
198                 275                 280                 285
199         Thr Leu Lys Asn Leu Glu Asp Leu Val Thr Glu Tyr Gln Gly Asn Phe
200             290                 295                 300
201         Ser Ala Trp Ser Gly Val Ser Lys Gly Leu Ala Glu Ser Leu Gln Pro
202         305                 310                 315                 320
203         Asp Tyr Ser Glu Arg Leu Cys His Val Ser Glu Ile Pro Pro Lys Gly
204                         325                 330                 335
205         Gly Glu Gly Pro Gly Gly Ser Pro Cys Ser Gln His Ser Pro Tyr Trp
206                     340                 345                 350
207         Ala Pro Pro Cys Tyr Thr Leu Lys Pro Glu Pro
208                 355                 360
209     <210> SEQ ID NO 4
210     <211> LENGTH: 733
211     <212> TYPE: DNA
212     <213> ORGANISM: Homo sapiens
213     <400> SEQUENCE: 4
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215           aattcgaggg tgcaccgtca gtcttcctct tccccccaaa acccaaggac accctcatga 120
216           tctcccggac tcctgaggtc acatgcgtgg tggtggacgt aagccacgaa gaccctgagg 180
217           tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca aagccgcggg 240
218           aggagcagta caacagcacg taccgtgtgg tcagcgtcct caccgtcctg caccaggact 300
219           ggctgaatgg caaggagtac aagtgcaagg tctccaacaa agccctccca acccccatcg 360
220           agaaaaccat ctccaaagcc aaagggcagc cccgagaacc acaggtgtac accctgcccc 420
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222           atccaagcga catcgccgtg gagtgggaga gcaatgggca gccggagaac aactacaaga 540
223           ccacgcctcc cgtgctggac tccgacggct ccttcttcct ctacagcaag ctcaccgtgg 600
224           acaagagcag gtggcagcag gggaacgtct tctcatgctc cgtgatgcat gaggctctgc 660
225           acaaccacta cacgcagaag agcctctccc tgtctccggg taaatgagtg cgacggccgc 720
226           gactctagag gat                                                   733
227     <210> SEQ ID NO 5
228     <211> LENGTH: 5
229     <212> TYPE: PRT
230     <213> ORGANISM: Homo sapiens
231     <220> FEATURE:
232     <221> NAME/KEY: SITE
233     <222> LOCATION: (3)
234     <223> OTHER INFORMATION: Xaa equals any amino acid
235     <400> SEQUENCE: 5
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237                 1               5
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239     <211> LENGTH: 86
240     <212> TYPE: DNA
241     <213> ORGANISM: Homo sapiens
242     <400> SEQUENCE: 6
243           gcgcctcgag atttccccga aatctagatt tccccgaaat gatttccccg aaatgatttc 60
              cccgaaatat ctgccatctc aattag                                      86
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY
PATENT APPLICATION **US/09/376,430A**

DATE: 04/06/2000
TIME: 11:23:37

Input Set: **I376430A.RAW**

Line	?	Error/Warning	Original Text
236	W	"N" or "Xaa" used: Feature required	Trp Ser Xaa Trp Ser
341	W	"N" or "Xaa" used: Feature required	Xaa Xaa Trp Xaa Xaa Trp Ser
356	W	"N" or "Xaa" used: Feature required	Thr Xaa Pro Ser Xaa Trp Ser
379	W	"N" or "Xaa" used: Feature required	Trp Xaa Xaa Xaa Pro Xaa Pro
390	W	"N" or "Xaa" used: Feature required	Ile Pro Xaa Val Pro Asp Pro
455	W	"N" or "Xaa" used: Feature required	Leu Trp Arg Xaa Lys Lys Phe Leu Xaa Pro S
457	W	"N" or "Xaa" used: Feature required	Ser Ile Phe Pro Gly Leu Phe Xaa Ile His G
505	W	"N" or "Xaa" used: Feature required	ctcmytccca gcgtgccaga cccgaaatcc atcttccc
546	W	"N" or "Xaa" used: Feature required	Thr Ser Gly Cys Leu Leu Asp Ala Xaa Gln A
552	W	"N" or "Xaa" used: Feature required	Gly Ile Arg Xaa Asp Gly Asp Val Phe Xaa T
579	W	"N" or "Xaa" used: Feature required	Trp Xaa Trp Ser

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/376,430A

DATE: 04/06/2000
TIME: 11:23:37

Input Set: I376430A.RAW

PREVIOUSLY ERRORED SEQUENCES-EDITED

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<212> DNA
<213> Homo sapiens
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gccatcatgg ggcggctggt tctg 144

O'Hara E.

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/376,430A

DATE: 04/05/2000
TIME: 12:22:09

Input Set: I376430A.RAW

This Raw Listing contains the General Information Section and those Sequences containing ERRORS.

Does Not Comply
Corrected Diskette Needed

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1   <110> Moore, Paul A.
2         Rosen, Craig A.
3         Ruben, Steven M.
4   <120> Cytokine Receptor Common Gamma Chain Like
5   <130> PF466P1
6   <140> US/09/376,430A
7   <141> 1999-08-18
8   <150> 60/086,505
9   <151> 1998-05-22
10  <150> 60/078,563
11  <151> 1998-03-19
12  <150> 09/263,626
13  <151> 1999-03-05
14  <150> PCT/US99/05068
15  <151> 1999-03-05
16  <160> 32
17  <170> PatentIn Ver. 2.0
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ERRORED SEQUENCES FOLLOW

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18  <210> 32
19  <211> 144
20  <212> DNA
21  <213> Homo sapiens
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24        cggctggttc tgccggttag atctgccatc atggggcggc tggttctgcc ggttagatct 120
25        gccatcatgg ggcggctggt tctg                                        144
E--> 26   1
27        14
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VERIFICATION SUMMARY
PATENT APPLICATION US/09/376,430A

DATE: 04/05/2000
TIME: 12:22:09

Input Set: I376430A.RAW

Line	?	Error/Warning	Original Text
26	E	Number of Bases conflict w/ Running Total 1	